

SEQUENCE LISTING

<110> Curtis, Rory A.J., Lora, Jose M.
<120> 46798, A HUMAN MATRIX METALLOPROTEINASE
AND USES THEREFOR

<130> MPI2001-014P1RCPl (M)

<150> 60/262,252

<151> 2001-01-16

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2310

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (317)...(1651)

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aaaccggcg acagtcctc tccgtgcggg ggcggcgag agcagtccca tccccgggtt 240
cccgccgcgg gctgactggc ggctgggtttc ctgcgcgcag tagctccccc agccggggctg 300
cacccggaggc ggcgag atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg 352
Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu
1 5 10

cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga 400
Gln Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly
15 20 25

ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga 448
Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly
30 35 40

tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc 496
Tyr Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser
45 50 55 60

gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc 544
Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly
65 70 75

gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg 592
Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly
80 85 90

gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gac		640	
Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp			
95	100	105	
ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca		688	
Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Arg Phe Ala			
110	115	120	
aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa		736	
Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu			
125	130	135	140
gcg cac ttc gac caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg		784	
Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly			
145	150	155	
cgc aac ctg ttc gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc		832	
Arg Asn Leu Phe Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly			
160	165	170	
ctc acc cac tcg ccc gcg cgc ctc atg gcg ccc tac tac tac aag		880	
Leu Thr His Ser Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys			
175	180	185	
agg ctg ggc cgc gac gcg ctg ctc aac tgg gac gac gtg ctg gcc gtg		928	
Arg Leu Gly Arg Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val			
190	195	200	
cag agc ctg tat ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc		976	
Gln Ser Leu Tyr Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu			
205	210	215	220
cca gga aag ctg ttc act gac ttt gag acc tgg gac tcc tac agc ccc		1024	
Pro Gly Lys Leu Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro			
225	230	235	
caa gga agg cgc cct gaa acg cag ggc cct aaa tac tgc cac tct tcc		1072	
Gln Gly Arg Arg Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser			
240	245	250	
ttc gat gcc atc act gta gac agg caa cag caa ctg tac att ttt aaa		1120	
Phe Asp Ala Ile Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys			
255	260	265	
ggg agc cat ttc tgg gag gtg gca gct gat ggc aac gtc tca gag ccc		1168	
Gly Ser His Phe Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro			
270	275	280	
cgt cca ctg cag gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct		1216	
Arg Pro Leu Gln Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala			
285	290	295	300
gcg gca gtg tca ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt		1264	
Ala Ala Val Ser Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly			
305	310	315	

cga tgc tgg agg ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag 1312
 Arg Cys Trp Arg Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln
 320 325 330

ctg tgc cgg gca ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc 1360
 Leu Cys Arg Ala Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe
 335 340 345

ttc cct cct ctg cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac 1408
 Phe Pro Pro Leu Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr
 350 355 360

gtg ctg gcc cga ggg gga ctg caa gtg gag ccc tac tac ccc cga agt 1456
 Val Leu Ala Arg Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser
 365 370 375 380

ctg cag gac tgg gga ggc atc cct gag gag gtc agc ggc gcc ctg cgg 1504
 Leu Gln Asp Trp Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro
 385 390 395

agg ccc gat ggc tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc 1552
 Arg Pro Asp Gly Ser Ile Ile Phe Phe Arg Asp Arg Tyr Trp Arg
 400 405 410

ctc gac cag gcc aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc 1600
 Leu Asp Gln Ala Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr
 415 420 425

gag ctg ccc tgg atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg 1648
 Glu Leu Pro Trp Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu
 430 435 440

ttc tgaaggcacc tcctcacctc agaaaactggt ggtgtctca gggcaaaatc 1701
 Phe
 445

atgtttccca cccccggggc agaacccttc ttagaagcct ctgagtccct ctgcagaaga 1761
 ccggcgacca aaggctccat ctggaaatct gtctgcctt gttcccttggaa gaatgcac 1821
 ttgtctttgt ctgtcccccac cacatggagg tggggggtggg atcaatctta gaaaaagcaa 1881
 aaaaagggttcc cagatccctt ggccctttcc tccggaggact tctatccctt ccaggcttt 1941
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 aggacccttc ggtctcgat tcgtaaaaacg gtgtcatatt tgcgtcaggagg ccccccccc 2121
 gggaaagcatg gatggggatg aaggcacaagg cgtctccaa cttcagggcc ctttgtgggg 2181
 tcaggacaca gagtggggagg gagatgtatc cttcagctgg tggggccgaga aaaaaaaaaa 2241
 gggtggggat aaagaggatgc aaaaaaaaaaaaaaaa aaaaaaaaaaaag 2310
 ggccggccgc

<210> 2
<211> 445
<212> PRT
<213> Homo sapiens

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Arg	Lys	Glu	Ala	Glu	Ala	Phe	Leu	Glu	Lys	Tyr	Gly	Tyr	Leu	Asn	Glu
35	40	45													
Gln	Val	Pro	Lys	Ala	Pro	Thr	Ser	Thr	Arg	Phe	Ser	Asp	Ala	Ile	Arg
50	55	60													
Ala	Phe	Gln	Trp	Val	Ser	Gln	Leu	Pro	Val	Ser	Gly	Val	Leu	Asp	Arg
65	70	75													
Ala	Thr	Leu	Arg	Gln	Met	Thr	Arg	Pro	Arg	Cys	Gly	Val	Thr	Asp	Thr
85	90	95													
Asn	Ser	Tyr	Ala	Ala	Trp	Ala	Glu	Arg	Ile	Ser	Asp	Leu	Phe	Ala	Arg
100	105	110													
His	Arg	Thr	Lys	Met	Arg	Arg	Lys	Lys	Arg	Phe	Ala	Lys	Gln	Gly	Gly
115	120	125													
Ala	Leu	Ala	His	Ala	Phe	Leu	Pro	Arg	Arg	Gly	Glu	Ala	His	Phe	Asp
130	135	140													
Gln	Asp	Glu	Arg	Trp	Ser	Leu	Ser	Arg	Arg	Gly	Arg	Asn	Leu	Phe	
145	150	155													
Val	Val	Leu	Ala	His	Glu	Ile	Gly	His	Thr	Leu	Gly	Leu	Thr	His	Ser
165	170	175													
Pro	Ala	Pro	Arg	Ala	Leu	Met	Ala	Pro	Tyr	Tyr	Lys	Arg	Leu	Gly	Arg
180	185	190													
Asp	Ala	Leu	Leu	Ser	Trp	Asp	Asp	Val	Leu	Ala	Val	Gln	Ser	Leu	Tyr
195	200	205													
Gly	Lys	Pro	Leu	Gly	Gly	Ser	Val	Ala	Val	Gln	Leu	Pro	Gly	Lys	Leu
210	215	220													
Phe	Thr	Asp	Phe	Glu	Thr	Trp	Asp	Ser	Tyr	Ser	Pro	Gln	Gly	Arg	Arg
225	230	235													
Pro	Glu	Thr	Gln	Gly	Pro	Lys	Tyr	Cys	His	Ser	Ser	Phe	Asp	Ala	Ile
245	250	255													
Thr	Val	Asp	Arg	Gln	Gln	Gln	Leu	Tyr	Ile	Phe	Lys	Gly	Ser	His	Phe
260	265	270													
Trp	Glu	Val	Ala	Ala	Asp	Gly	Asn	Val	Ser	Glu	Pro	Arg	Pro	Leu	Gln
275	280	285													
Glu	Arg	Trp	Val	Gly	Leu	Pro	Pro	Asn	Ile	Glu	Ala	Ala	Ala	Val	Ser
290	295	300													
Leu	Asn	Asp	Gly	Asp	Phe	Tyr	Phe	Phe	Lys	Gly	Gly	Arg	Cys	Trp	Arg
305	310	315													
Phe	Arg	Gly	Pro	Lys	Pro	Val	Trp	Gly	Leu	Pro	Gln	Leu	Cys	Arg	Ala
325	330	335													
Gly	Gly	Leu	Pro	Arg	His	Pro	Asp	Ala	Ala	Leu	Phe	Phe	Pro	Pro	Leu
340	345	350													
Arg	Arg	Leu	Ile	Leu	Phe	Lys	Gly	Ala	Arg	Tyr	Tyr	Val	Leu	Ala	Arg
355	360	365													
Gly	Gly	Leu	Gln	Val	Glu	Pro	Tyr	Tyr	Pro	Arg	Ser	Leu	Gln	Asp	Trp
370	375	380													
Gly	Gly	Ile	Pro	Glu	Glu	Val	Ser	Gly	Ala	Leu	Pro	Arg	Pro	Asp	Gly
385	390	395													
Ser	Ile	Ile	Ile	Phe	Arg	Asp	Asp	Arg	Tyr	Trp	Arg	Leu	Asp	Gln	Ala
405	410	415													
Lys	Leu	Gln	Ala	Thr	Thr	Ser	Gly	Arg	Ala	Thr	Glu	Leu	Pro	Trp	
420	425	430													
Met	Gly	Cys	Trp	His	Ala	Asn	Ser	Gly	Ser	Ala	Leu	Phe			
435	440	445													

<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1335)

<400> 3

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tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg
20 25 30
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa
35 40 45
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga
50 55 60
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc
65 70 75 80
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc
85 90 95
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga
100 105 110
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc
115 120 125
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly

gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac
130 135 140 140
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp

caa gat gag cgc tgg tcc ctg agc cgc cgc ggg cgc aac ctg ttc
145 150 155 160
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Gly Arg Asn Leu Phe

gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tcg
165 170 175
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser

ccc gcg ccc cgc ggc ctc atg gcg ccc tac tac aag agg ctg ggc cgc
180 185 190

Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
gac ggc ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat
195 200 205
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg
210 215 220
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc
225 230 235 240
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc
245 250 255
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc
260 265 270
Thr Val Asp Arg Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
tgg gag gtg gca gct gat ggc aac gtc tca gag ccc cgt cca ctg cag
275 280 285
Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca
290 295 300
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg
305 310 315 320
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Arg Cys Trp Arg
ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca
325 330 335
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc ctc cct cct ctg
340 345 350
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga
355 360 365
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
ggg gga ctg caa gtg gag ccc tac ccc cga agt ctg cag gac tgg
370 375 380
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc
385 390 395 400
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc
405 410 415

Ser Ile Ile Phe Phe Arg Asp Asp Arg Arg Tyr Trp Arg Leu Asp Gln Ala
aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg
420 425 430
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc
435 440 445
Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe

<210> 4
<211> 171
<212> PRT
<213> Artificial sequence

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Thr Arg Lys Lys Ala Ser Asn Ser Leu Val Glu Lys Leu Lys Glu Met
20 25 30
Gln Lys Phe Phe Gly Leu Pro Val Thr Gly Lys Leu Asp Ser Asn Thr
35 40 45
Leu Glu Val Met Lys Lys Pro Arg Cys Gly Val Pro Asp Val Gly Glu
50 55 60
Phe Arg Thr Phe Pro Gly Ser Pro Lys Trp Ser Lys Asn Asn Leu Leu
65 70 75 80
Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Glu Asp Val
85 90 95
Asp Asp Ala Ile Arg Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro
100 105 110
Leu Thr Phe Thr Arg Val Ser Asp Gly Glu Ala Asp Ile Met Ile Ser
115 120 125
Phe Ala Arg Gly Glu His Gly Asp Phe Tyr Pro Phe Asp Gly Lys Gly
130 135 140
Gly Leu Leu Ala His Ala Phe Ala Pro Gly Pro Gly Ile Gly Ile Gly
145 150 155 160
Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
165 170

<210> 5
<211> 50
<212> PRT
<213> Homo sapiens

<400> 5
Ile Asp Ala Ala Phe Glu Asp Arg Asp Arg Gly Lys Thr Tyr Phe Phe
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Lys Gly Asp Lys Tyr Trp Arg Phe Asp Pro Glu Thr Arg Gln Arg Val
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Asp Pro Gly Tyr Pro Lys Leu Ile Ser Asp Leu Trp Pro Asp Gly Leu
35 40 45
Pro Cys
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<210> 6
<211> 471

<212> PRT
<213> Homo sapiens

<400> 6
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Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser
20 25 30
Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
35 40 45
Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
50 55 60
Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
65 70 75 80
Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
85 90 95
Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
100 105 110
Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
115 120 125
Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
130 135 140
Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
145 150 155 160
Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr
165 170 175
Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly
180 185 190
Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
195 200 205
Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
210 215 220
Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
225 230 235 240
Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
245 250 255
Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
260 265 270
Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
275 280 285
Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
290 295 300
Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
305 310 315 320
Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
325 330 335
Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
340 345 350
Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
355 360 365
Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
370 375 380
Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
385 390 395 400
Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
405 410 415
Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp

420 425 430
Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
435 440 445
Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
450 . 455 460
Ala Asn Ser Ile Leu Trp Cys
465 470

<211> <210> 7

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)...(1)

<223> The amino acid at position 1 can be G, S, T, A, L,
I, V, N.

<223> Xaa at position 2 and 3 = any amino acid

<221> VARIANT

<222> (6)...(6)

<223> The amino acid at position 6 can be L, I, V, M, F,
Y, W.

<221> VARIANT

<222> (7)...(7)

<223> The amino acid at position 7 can not be D, E, H,
R, K, P.

<223> Xaa at position 9= any amino acid

<221> VARIANT

<222> (10)...(10)

<223> The amino acid at position 10 can be L, I, V, M,
F, Y, W, G, S, P, Q.

<400> 4

Xaa Xaa Xaa His Glu Xaa Xaa His Xaa Xaa

1

5

10

<210> 8

<211> 2527

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (300)...(1862)

<400> 8

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gcggacccgc gggcaggcac tgcccgccgt ggacgacgtc tggccggctc cccgcgaagg 120
gcagcggagg agcggcccaag agcgcgcagc tagggcactg gcaaaccaccc gggacagtcc 180

ctctccgtgc	ggggcgccgc	cagacgactc	ccatccccgg	ggtcccgggc	gcggctgact	240
gccggctgg	tccctgcgcg	cagtagctcc	ccgaggccgg	ctgcaccgga	ggcggcgag	299
atg gtc	gag cgc gtc	ggc ctc ctg	ctg cgc ctc	ctg cag ctg	ctg cta ctg	347
Met Val Ala Arg Val	Gly Leu Leu Leu	Arg Ala Leu Gln	Leu Leu Leu			
1	5	10	15			
tgg ggc cac	ctg gac gcc	cag ccc gag	cgc gga ggc	cag gag ctg		395
Trp Gly His	Leu Asp Ala	Gln Pro Ala	Glu Arg Gly	Gly Gln Glu	Leu	
20	25	30				
cgc aag gag	gag gca ttc	cta gag aag	tac gga tac	ctc aat gaa		443
Arg Lys	Glu Ala Glu	Ala Phe	Leu Glu Lys	Tyr Gly Tyr	Leu Asn Glu	
35	40	45				
cag gtc ccc	aaa gct ccc acc	tcc act cga	ttc agc gat	gcc atc aga		491
Gln Val	Pro Lys	Ala Pro	Thr Ser Thr	Arg Phe Ser	Asp Ala Ile Arg	
50	55	60				
gcg ttt cag	tgg gtg tcc	cag cta cct	gtc agc ggc	gtg ttg gac	cgc	539
Ala Phe	Gln Trp Val	Ser Gln Leu	Pro Val Ser	Gly Val Leu	Asp Arg	
65	70	75	80			
gcc acc ctg	cgc cag atg	act cgt ccc	cgc tgc ggg	gtt aca gat	acc	587
Ala Thr	Leu Arg Gln	Met Thr Arg	Pro Arg Cys	Gly Val Thr	Asp Thr	
85	90	95				
aac agt tat	gct gcc tgg	gct gag agg	atc agt gac	ttt gtt aca	gtt	635
Asn Ser Tyr	Ala Ala Trp	Ala Glu Arg	Ile Ser Asp	Leu Phe	Ala Arg	
100	105	110				
cac cgg acc	aaa atg agg	cgt aag aaa	cgc ttt gca	aag caa ggt	aac	683
His Arg	Thr Lys Met	Arg Arg Lys	Lys Arg Phe	Ala Lys Gln	Gly Asn	
115	120	125				
aaa tgg tac	aag cag cac	ctc tac cgc	ctg gtg aac	tgg cct gag		731
Lys Trp Tyr	Lys Gln His	Leu Ser Tyr	Arg Leu Val	Asn Trp Pro	Glu	
130	135	140				
cat ctg ccg	gag ccg gca	gtt cgg ggc	gcc gtg cgc	gcc gcc ttc	cag	779
His Leu Pro	Glu Pro Ala	Val Arg Gly	Ala Val Arg	Ala Ala Phe	Gln	
145	150	155	160			
ttg tgg agc	aac gtc tca	gct ctg gag	ttc tgg gag	gcc cca gca	gca	827
Leu Trp Ser	Asn Val Ser	Ala Leu Glu	Phe Trp Glu	Ala Pro Ala	Thr	
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Gly Pro Ala	Asp Ile Arg	Leu Thr Phe	Phe Gln Gly	Asp His Asn	Asp	
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Gly Leu Gly	Asn Ala Phe	Asp Gly Pro	Gly Ala Leu	Ala His Ala		
195	200	205				
ttc ctg ccc	cgc cgc ggc	gaa gcg cac	ttc gac caa	gat gag cgc	tgg	971
Phe Leu Pro	Arg Arg Gly	Glu Ala His	Phe Asp Gln	Asp Glu Arg	Trp	
210	215	220				

145	150	155	160
Leu Trp Ser Asn Val	Ser Ala Leu Glu Phe	Trp Glu Ala Pro Ala Thr	
165	170	175	
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp			
180	185	190	
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala			
195	200	205	
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp			
210	215	220	
Ser Leu Ser Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His			
225	230	235	240
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala			
245	250	255	
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser			
260	265	270	
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly			
275	280	285	
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu			
290	295	300	
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly			
305	310	315	320
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln			
325	330	335	
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala			
340	345	350	
Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly			
355	360	365	
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp			
370	375	380	
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys			
385	390	395	400
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg			
405	410	415	
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu			
420	425	430	
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Leu Gln Val			
435	440	445	
Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu			
450	455	460	
Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe			
465	470	475	480
Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr			
485	490	495	
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His			
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Ala Asn Ser Gly Ser Ala Leu Phe			
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gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg cgc cgc		1067
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala		
245 250 255		
ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc		1115
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser		
260 265 270		
tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg		1163
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly		
275 280 285		
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Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu		
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acc tgg gac tcc tac agc ccc caa gga agg cgc cct gaa acg cag ggc		1259
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly		
305 310 315 320		
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Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln		
325 330 335		
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Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala		
340 345 350		
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Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly		
355 360 365		
ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat		1451
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp		
370 375 380		
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Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys		
385 390 395 400		
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Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg		
405 410 415		
cat cct gac gcc gcc ctc ttc ctc cct ctg cgc cgc ctc atc ctc		1595
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu		
420 425 430		
ttc aag ggt gcc tac tac gtg ctg gcc cga ggg gga ctg caa gtg		1643
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Leu Gln Val		
435 440 445		

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Ser	Leu	Ser	Arg	Arg	Arg	Gly	Arg	Asn	Leu	Phe	Val	Val	Leu	Ala	His		
225			230						235						240		
gag	atc	ggt	cac	acg	ctt	ggc	ctc	acc	cac	tcg	ccc	gcg	ccg	cgc	gcg		768
Glu	Ile	Gly	His	Thr	Leu	Gly	Leu	Thr	His	Ser	Pro	Ala	Pro	Arg	Ala		
245				250					255							255	
ctc	atg	gcf	ccc	tac	tac	aag	agg	ctg	ggc	cgc	gac	gcf	ctg	ctc	agc		816
Leu	Met	Ala	Pro	Tyr	Tyr	Lys	Arg	Leu	Gly	Arg	Asp	Ala	Leu	Leu	Ser		
			260					265				270					
tgg	gac	gac	gtg	ctg	gcc	gtg	cag	agc	ctg	tat	ggg	aag	ccc	cta	ggg		864
Trp	Asp	Asp	Val	Leu	Ala	Val	Gln	Ser	Leu	Tyr	Gly	Lys	Pro	Leu	Gly		
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ggc	tca	gtg	gcc	gtc	cag	ctc	cca	gga	aag	ctg	ttc	act	gac	ttt	gag		912
Gly	Ser	Val	Ala	Val	Gln	Leu	Pro	Gly	Lys	Leu	Phe	Thr	Asp	Phe	Glu		
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Thr	Trp	Asp	Ser	Tyr	Ser	Pro	Gln	Gly	Arg	Arg	Pro	Glu	Thr	Gln	Gly		
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cct	aaa	tae	tgc	cac	tct	tcc	tcc	gat	gcc	att	act	act	gta	gac	agg	caa	1008
Pro	Lys	Tyr	Cys	His	Ser	Ser	Phe	Asp	Ala	Ile	Thr	Val	Asp	Arg	Gln		
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cag	caa	ctg	tac	att	ttt	aaa	ggg	agc	cat	ttc	tgg	gag	gtg	gca	gct		1056
Gln	Gln	Leu	Tyr	Ile	Phe	Lys	Gly	Ser	His	Phe	Trp	Glu	Val	Ala	Ala		
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Asp	Gly	Asn	Val	Ser	Glu	Pro	Arg	Pro	Leu	Gln	Glu	Arg	Trp	Val	Gly		
			355				360			365							
ctg	ccc	ccc	aac	att	gag	gct	gcf	gca	gtg	tca	ttg	aat	gat	gga	gat		1152
Leu	Pro	Pro	Asn	Ile	Glu	Ala	Ala	Ala	Val	Ser	Leu	Asn	Asp	Gly	Asp		
			370				375			380							
ttc	tac	ttc	aaa	ggg	ggg	ggt	cga	tgc	tgc	tgg	agg	ttc	cgf	ggc	ccc	aag	1200
Phe	Tyr	Phe	Phe	Lys	Gly	Gly	Arg	Cys	Trp	Arg	Phe	Arg	Gly	Pro	Lys		
			385				390			395			400				
cca	gtg	tgg	ggg	gtt	ctc	cca	cag	ctg	tgc	cgg	ggg	ctg	ccc	cgc		1248	
Pro	Val	Trp	Gly	Leu	Pro	Gln	Leu	Cys	Arg	Ala	Gly	Gly	Leu	Pro	Arg		
			405				410			415							
cat	cct	gac	gcc	gcc	ctc	ttc	ttc	cct	ctg	cgc	cgc	ctc	atc	ctc		1296	
His	Pro	Asp	Ala	Ala	Leu	Phe	Phe	Pro	Pro	Leu	Arg	Arg	Leu	Ile	Leu		
			420				425			430							
ttc	aag	ggt	gcc	cgc	tac	tac	gtg	ctg	gcc	cga	ggg	gga	ctg	caa	gtg		1344
Phe	Lys	Gly	Ala	Arg	Tyr	Tyr	Val	Leu	Ala	Arg	Gly	Gly	Leu	Gln	Val		
			435				440			445							

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Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
450 455 460

gag gtc agc ggc gcc ctg ccg agg ccc gat ggc tcc atc atc ttc ttc 1440
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465 470 475 480

cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc 1488
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485 490 495

acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat 1536
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
500 505 510

gcc aac tcg ggg agc gcc ctg ttc tga 1563
Ala Asn Ser Gly Ser Ala Leu Phe *

515 520